Bifunctional Protein, Preparation and Use

The present invention relates to a bifunctional protein capable of directing a host cell producing said protein to specifically recognize selected target cells. Furthermore, the invention provides a method for the preparation of said protein, a DNA construct encoding said protein, a composition comprising a host cell expressing said DNA, and antibodies specifically recognizing said protein. Additionally, the invention relates to the use of such a host cell, e.g. for selectively killing tumor cells in vitro or in vivo.

The principle of adoptive immunotherapy, also referred to as cellular immunotherapy, is the transfer of immunologically active cells to a mammal in order to enhance the mammal's immune response to a disease state. To this end the immune cells are removed e.g. from the human patient or another subject, cultured, optionally in the presence of immunoenhancing agents such as interleukin 2, and subsequently (re-)administered to the patient, conventionally in the presence of an immunoenhancing agent. In the patient, the immunologically active cells act to alleviate the disease state.

Immunologically active cells suggested for adoptive immunotherapy include lymphokine activated killer (LAK) cells, derived from natural killer (NK) cells, and in vitro sensitized lymphocytes (IVS), derived from cytolytic or cytotoxic T lymphocytes (CTL), also referred to as killer T lymphocytes. LAK cells are cytolytic cells which react with a broad spectrum of target cells. They are not major histocompatibility complex (MHC)-restricted and capable of lysing tumor cells, but also normal cells in vitro. CTL have clonal specificities, i.e. each clone is specific for a particular antigenic structure on the surface of a target cell. A particular CTL recognizes and binds a unique antigen and thus becomes activated and can then multiply and destroy the target cells. The recognition process is MHC-restricted and dependent, since an antigen is recognized only in association with one of the self class I MHC surface molecules expressed by the target cell.

Recognition of a specific antigen by T cells is mediated by the T-cell antigen receptor (TCR) (A. Weiss, Cell 73, 209-212 (1993)). Binding of a ligand to the receptor may trigger cellular effector programs, such as activation of tyrosine kinases, intracellular calcium ion release and interleukin 2 production (R.T. Abraham et al., Trends Biochem. Sci. 17, 434-438 (1992)).

The TCR is a multimeric surface complex comprising the products of at least six genes, all

of which are required for efficient plasma membrane expression. The clonotypic alpha (α) and beta (β) chains of the TCR mediate specific target cell recognition. These chains are non-covalently associated with the non-polymorphic components of the CD3 complex gamma (γ), delta (δ), and epsilon (ϵ), and the zeta (ζ) chain. The disulfid-linked ζ homodimer is a transmembrane molecule and its cytoplasmic part plays a central role in the TCR-mediated signal transduction and induction of cytolysis. The ζ chain is capable of autonomous signal transduction, i.e. ζ alone is sufficient to mediate a response. Fusion of the ζ chain with an extracellular ligand binding domain may result in a molecule which can be activated by interaction with the ligand (S.J. Frank et al., Science 249, 174-177 (1990); C. Romeo & B. Seed, Cell 64, 1037-1046 (1990); F. Letourneur & R.D. Klausner, Proc. Natl. Acad. Sci. USA 88, 8905-8909 (1991)). An isoform of ζ, eta (η), represents an alternatively spliced form of the ζ gene transcript.

Tumor formation involves the mutation of oncogenes and tumor suppressor genes in somatic cells. Such mutations may result in structural alterations or in the overexpression of proteins. Both events might lead to alterations in the intracellular processing of these proteins and the presentation of new antigenic structures in association with the major histocompatibility antigens on the surface of the cells. The detection of antibodies directed against oncogene products in the serum of tumor patients is an indication that oncogene products can be antigenic. Further evidence for this antigenicity is the evocation of the cellular immune response. The occurrence of CTL which recognize and eliminate tumor cells has been demonstrated in a number of model systems (T. Boon, Adv. Cancer Res. 58, 177-210 (1992); M.W. Kast et al., Cell 59, 603-614 (1989); Disis et al., Cancer Res. 54, ? 16-20 (1994)).

Present strategies aimed at exploiting the cytolytic activity of T-lymphocytes, e.g. for the treatment of cancer, suffer from several shortcomings, such as MHC-restriction of the recognition process in naturally occurring CTL. There is a need for an approach to overcome the limitations currently encountered.

It is the object of the present invention to provide such an improved approach involving manipulation of CTL-recognition specificity, e.g.to make the altered CTL potent and selective anti-tumor agents. This approach is based on the identification of consistent genetic alterations in benign and particularly in malignant tumor cells. Providing CTL with a defined tumor cell specificity enables the targeting to defined tumor cells and MHC-unrestricted and MHC-independent destruction of said target cells. Tumor cell lysis

by CTL grafted with a novel, MHC independent recognition specificity may be exploited in vitro (ex vivo) or in vivo, e.g. in a gene therapy approach involving cancer treatment.

The tumor cells are (pre-)defined or selected target cells in that they carry the antigenic structure (ligand) recognized and bound by the antigen binding domain which is part of the chimeric protein of the invention.

The present invention concerns a chimeric protein capable of directing a CTL to specifically recognize and kill selected tumor cells. More specifically, the present invention provides a chimeric protein comprising a recognition function, a hinge region and the ζ chain of the TCR, and a CTL producing one or more of such protein molecules. Binding of a cell-bound ligand to the recognition part of the chimeric protein of the invention leads to ζ chain-mediated signal transduction within the CTL and eventually results in the lysis of the cell carrying the ligand.

The chimeric protein of the invention is a protein which does not exist in nature. The protein is bifunctional in that it is capable of both specifically recognizing and binding to a particular antigenic structure (via its recognition function domain) and serving as a signalling component (via the ζ chain part). The hinge region serves as a spacer and ensures the necessary accessibility and flexibility of the recognition function domain. The hinge region is understood to be essential for the functionality of the chimeric protein of the invention. Preferably, the arrangement within the chimeric protein is such that the recognition function is located at the N-terminus and linked to the ζ chain part at the C-terminus of the chimeric protein via the hinge region. Being a cell surface receptor molecule the chimeric protein of the invention comprises an extracellular domain, a transmembrane domain and a cytoplasmic domain and is inserted into the plasma membrane of the host cell, e.g. the CTL. The functionality of the protein of the invention within the host cell is detectable in an assay suitable for demonstrating the signalling potential of said protein upon binding of a particular ligand, e.g. in an assay enabling detection of a signalling pathway triggerred upon binding of the ligand, such as an assay involving measurement of the increase of calcium ion release, intracellular tyrosine phosphorylation, inositol phosphate turnover or interleukin (IL) 2, interferon γ, GM-CSF, IL-3, IL-4 production thus effected. (R.T. Abraham et al., Trend Biochem. Sci. 17, 434-438 (1992)). Such assays are readily available to the person with ordinary skill in the art. Reference is made to the assays employed in the Examples. It is evident that these assays may be modified, e.g. by using other suitable cell lines.

The recognition function is contributed by an antigen binding domain of an antibody, particularly a single chain antibody (scFv). Single chain antibodies are gene fusions comprising the variable domains of the heavy and light chain of monoclonal antibodies. Said recognition and binding function is conferred to the ζ-chain of the TCR-complex to circumvent MHC-restricted antigen recognition through the α/β chains of the TCR.

The antigen binding domain is derivable from a monoclonal antibody directed against and specific for a suitable antigen on a tumor cell.

A suitable antigen is an antigen with enhanced or specific expression on the surface of a tumor cell as compared to a normal cell, e.g. an antigen evolving from consistent genetic alterations in tumor cells. Examples of suitable antigens include ductal-epithelial mucine, gp 36, TAG-72, growth factor receptors and glycosphingolipids and other carbohydrate antigens preferentially expressed in tumor cells (Please give references for the below captioned antigens and antibodies). Ductal-epithelial mucine is enhancedly expressed on breast, ovarian and pancreas carcinoma cells and is recognized e.g. by monoclonal antibody SM3 (Zotter et al., Cancer Rev. 11, 55-101 (1988)). The glycoprotein gp 36 is found on the surface of human leukemia and lymphoma cells. An exemplary antibody recognizing said antigen is SN 10. TAG-72 is a pancarcinoma antigen recognized by monoclonal antibody CC49 (Longenecker, Sem. Cancer Biol. 2, 355-356). Growth factor receptors are e.g. the human epidermal growth factor (EGF) receptor (Khazaie et al., Cancer and Metastasis Rev. 12, 255-274 (1993)) and HER2, also referred to as erbB-2 or gp 185 (A. Ullrich and J. Schlessinger, Cell 61, 203-212 (1990)). The erbB-2 receptor is a transmembrane molecule which is overexpressed in a high percentage of human carcinomas (N.E. Hynes, Sem. in Cancer Biol. 4, 19-26 (1993)). Expression of erbB-2 in normal adult tissue is low. This difference in expression identifies the erbB-2 receptor as "tumor enhanced".

Preferably, the antigen binding domain is obtainable from a monoclonal antibody produced by using as immunogen viable human tumor cells presenting the antigen in its native form. In a preferred embodiment of the invention, the recognition part of the chimeric protein specifically binds to an antigenic determinant on the extracellular domain of a growth factor receptor, particularly HER 2. Monoclonal antibodies directed to the HER2 growth factor receptor are known and are described, for example, by S.J. Mc Kenzie et al., Oncogene 4, 543-548 (1990), R.M. Hudziak et al., Molecular and

Cellular Biology 9, 1165-1172 (1989), International Patent Application WO 89/06692 (Genentech) and Japanese Patent Application Kokai 02-150 293 (Ajinomoto KK). Monoclonal antibodies raised against viable human tumor cells presenting HER2 in its native form, such as SKBR3 cells, are described, for example, in European patent application EP-A-502 812 (Ciba-Geigy) which is enclosed herein by reference, and include antibodies FRP5, FSP16, FSP77 and FWP51. Hybridoma cell lines producing these antibodies have been deposited with the European Collection of Animal Cell Cultures (ECACC, PHLS Centre for Applied Microbiology & Research, Porton Down, Salisbury, UK) on November 21, 1990 under accession numbers 90112115, 90112116, 90112117 and 90112118, respectively.

In the chimeric protein of the invention, the preferred antigen binding domain is a single-chain recombinant antibody (scFv) comprising the light chain variable domain (V_L) bridged to the heavy chain variable domain (V_H) via a flexible linker (spacer), preferably a peptide. Advantageously, the peptide consists of about 10 to about 30 amino acids, particularly naturally occurring amino acids, e.g. about 15 naturally occurring amino acids. Preferred is a peptide consisting of amino acids selected from L-glycine and L-serine, in particular the 15 amino acid peptide consisting of three repetitive units of Gly-Gly-Gly-Gly-Ser. Advantageous is a single-chain antibody wherein V_H is located at the N-terminus of the recombinant antibody. Preferred is a chimeric protein wherein the single-chain recombinant antibody has an above-defined preferred specificity, e.g. a chimeric protein comprising a single-chain recombinant antibody wherein the heavy chain variable domain and the light chain variable domain are derivable from a monoclonal antibody, e.g. a murine monoclonal antibody, directed to the human growth factor receptor HER2, such as a murine monoclonal antibody selected from the group consisting of FSP16, FSP77, FRP5 and FWP51.

The variable domain of an antibody heavy or light chain consists of so-called framework regions (FRs), which are fairly conserved in antibodies with different specificities, and of hypervariable regions also called complementarity determining regions (CDRs), which are typical for a particular specificity. In the antigen binding domain of a chimeric protein according to the invention, preferably the FRs are derivable from a mammalian, e.g. a murine or particularly a human antibody. The scFv derivative of a monoclonal antibody is grafted onto the ζ chain of the TCR/CD3 complex.

Particularly preferred is a chimeric protein comprising a single-chain recombinant

antibody wherein the heavy chain variable domain comprises a polypeptide of the formula

$$FR_1\text{-}CDR_{1H}\text{-}FR_2\text{-}CDR_{2H}\text{-}FR_3\text{-}CDR_{3H}\text{-}FR_4 \qquad (I)$$

Seq ID NO : 2

wherein the polypeptide chain is described as starting at the N-terminal extremity and ending at the C-terminal extremity and FR_1 is a peptide residue comprising at least 25-29, preferably 25-33 naturally occurring amino acids, FR_2 is a peptide residue comprising 12-16 naturally occurring amino acids, FR_3 is a peptide residue comprising 30-34 naturally occurring amino acids, FR_4 is a peptide residue comprising at least 6-10, preferably 6-13 naturally occurring amino acids, CDR_{1H} is a peptide residue of the amino acid sequence 31 to 35 of SEQ ID NO:2, CDR_{2H} is a peptide residue of the amino acid sequence 50 to 66 of SEQ ID NO:2, and CDR_{3H} is a peptide residue of the amino acid sequence 99 to 108 of SEQ ID NO:2, or, CDR_{1H} is a peptide residue of the amino acid sequence 31 to 35 of SEQ ID NO:4, CDR_{2H} is a peptide residue of the amino acid sequence 50 to 66 of SEQ ID NO:4, and CDR_{3H} is a peptide residue of the amino acid sequence 99 to 109 of SEQ ID NO:4, and wherein the amino acid Cys may be in the oxidized state forming S-S-bridges. These particular complementarity determining regions are Asn-Tyr-Gly-Met-Asn (CDR_{1H}), Trp-Ile-Asn-Thr-Ser-Thr-Gly-Glu-Ser-Thr-Phe-Ala-Asp-Asp-Phe-Lys-Gly (CDR_{2H}), and Trp-Glu-Val-Tyr-His-Gly-Tyr-Val-Pro-Tyr (CDR_{3H}) according to SEQ ID NO:2, or Ser-Tyr-Trp-Met-Asn (CDR_{1H}), Met-Ile-Asp-Pro-Ser-Asp-Ser-Glu-Thr-Gln-Tyr-Asn-Gln-Met-Phe-Lys-Asp (CDR_{2H}) and Gly-Gly-Ala-Ser-Gly-Asp-Trp-Tyr-Phe-Asp-Val (CDR_{3H}) according to SEQ. ID NO:4.

Especially preferred is a chimeric protein wherein the recombinant single-chain antibody comprises a heavy chain variable domain of formula I, wherein the framework regions FR_1, FR_2, FR_3 and FR_4 are those preferably derivable from a mammalian, especially a murine or a human antibody.

In a first embodiment of the invention, most preferred is a chimeric protein wherein the heavy chain variable domain of the recombinant single-chain antibody comprises a polypeptide of the amino acid sequence 2 to 120, of SEQ ID NO:2, wherein optionally one or more, e.g. 1, 2, 3 or 4, single amino acids within the amino acid sequences 2 to 30 (FR_1), 36 to 49 (FR_2), 67 to 98 (FR_3), and/or 110 to 120 (FR_4), are replaced by other amino acids or deleted, and wherein the amino acid Cys may be in the oxidized state forming S-S-bridges, in particular a chimeric protein wherein the heavy chain variable domain comprises a polypeptide of the amino acid sequence 6 to 119 of SEQ ID NO:2,

wherein the amino acid Cys may be in the oxidized state forming S-S-bridges.

In a second embodiment of the invention, most preferred is a chimeric protein wherein the heavy chain variable domain of the recombinant single-chain antibody comprises a polypeptide of the amino acid sequence 2 to 120 of SEQ ID NO:4, wherein optionally one or more, e.g. 1, 2, 3 or 4, amino acids within the amino acid sequences 2 to 30 (FR_1), 36 to 49 (FR_2), 67 to 98 (FR_3), and/or 110 to 120 (FR_4), are replaced with other amino acids or deleted, and wherein the amino acid Cys may be in the oxidized state forming S-S-bridges, in particular the recombinant antibodies with a heavy chain variable domain comprising a polypeptide of the amino acid sequence 6 to 120 of SEQ ID NO:4, wherein the amino acid Cys may be in the oxidized state forming S-S-bridges.

For example, a hydrophobic amino acid within a framework region may be replaced by another amino acid, preferably also a hydrophobic amino acid, e.g. a homologous amino acid, replaced with two amino acids (resulting in the insertion of an amino acid), or deleted. Likewise, a hydrophilic amino acid within a framework region may be replaced with another amino acid, two amino acids or deleted, whereby replacing amino acids preferably maintain the hydrogen bond structure of the corresponding framework region. Advantageously, any replacement of one or more amino acids takes into account the guidelines known in the art for reshaping or humanizing of an antibody. Particularly noteworthy are guidelines aimed at reducing the immunogenicity of the reshaped antibody (as compared to the "original" monoclonal antibody) and/or at designing an antibody which about equals or exceeds the binding affinity of the "original" antibody. A modification of amino acids may be confined to a single FR, i.e. FR_1, FR_2, FR_3 or FR_4, or involve two, three or all four of the FRs.

A likewise preferred chimeric protein of the invention comprises a recombinant single-chain antibody wherein the light chain variable domain comprises a polypeptide of the formula

$$FR_6\text{-}CDR_{1L}\text{-}FR_7\text{-}CDR_{2L}\text{-}FR_8\text{-}CDR_{3L}\text{-}FR_9 \qquad \text{(II)}$$

wherein the polypeptide chain is described as starting at the N-terminal extremity and ending at the C-terminal extremity and FR_6 is a peptide residue comprising naturally occurring amino acids, preferably 19-25, especially 19-23 naturally occurring amino acids, FR_7 is a peptide residue comprising 13-17 naturally occurring amino acids, FR_8 is a

peptide residue comprising 30-34 naturally occurring amino acids, FR_9 is a peptide residue comprising naturally occurring amino acids, particularly 7-11 naturally occurring amino acids, and CDR_{1L} is a peptide residue of the amino acid sequence 158 to 168 of SEQ ID NO:2, CDR_{2L} is a peptide residue of the amino acid sequence 184 to 190 of SEQ ID NO:2, and CDR_{3L} is a peptide residue of the amino acid sequence 223 to 231 of SEQ ID NO:2, or CDR_{1L} is a peptide residue of the amino acid sequence 159 to 164 of SEQ ID NO:4, CDR_{2L} is a peptide residue of the amino acid sequence 185 to 191 of SEQ ID NO:4, and CDR_{3L} is a peptide residue of the amino acid sequence 224 to 231 of SEQ ID NO:4, and wherein the amino acid Cys may be in the oxidized state forming S-S-bridges. These particular complementarity determining regions are Lys-Ala-Ser-Gln-Asp-Val-Tyr-Asn-Ala-Val-Ala (CDR_{1L}), Ser-Ala-Ser-Ser-Arg-Tyr-Thr (CDR_{2L}), and Gln-Gln-His-Phe-Arg-Thr-Pro-Phe-Thr (CDR_{3L}) according to SEQ ID NO:2, or Lys-Ala-Ser-Gln-Asp-Ile-Lys-Lys-Tyr-Ile-Ala (CDR_{1L}), Tyr-Thr-Ser-Val-Leu-Gln-Pro (CDR_{2L}) and Leu-His-Tyr-Asp-Tyr-Leu-Tyr-Thr (CDR_{3L}) according to SEQ ID NO:4.

Especially preferred is a chimeric protein wherein the recombinant antibody comprises a light chain variable domain of formula II, wherein the peptide residues of the framework regions FR_5, FR_6, FR_7 and FR_8 are those derivable from a mammalian, especially a murine or a human, antibody.

In one embodiment of the invention, most preferred is a chimeric protein wherein the recombinant antibody comprises a light chain variable domain comprising a polypeptide of the amino acid sequence 135 to 240 of SEQ ID NO:2, wherein optionally one or more, e.g. 1, 2, 3 or 4, amino acids within the amino acid sequences 135 to 157 (FR_6), 169 to 183 (FR_7), 191 to 222 (FR_8), and/or 232 to 240 (FR_9) are replaced by other amino acids or deleted, and wherein the amino acid Cys may be in the oxidized state forming S-S-bridges, in particular a light chain variable domain comprising a polypeptide of the amino acid sequence 135 to 240 of SEQ ID NO:2, wherein the amino acid Cys may be in the oxidized state forming S-S-bridges.

In a second embodiment of the invention, most preferred is a chimeric protein wherein the recombinant antibody comprises a light chain variable domain comprising a polypeptide of the amino acid sequence 136 to 240 of SEQ ID NO:4, wherein optionally one or more, e.g. 1, 2, 3 or 4 single amino acids within the amino acid sequences 136 to 158 (FR_6), 170 to 184 (FR_7), 192 to 223 (FR_8), and/or 232 to 240 (FR_9) are replaced by other amino acids or deleted, and wherein the amino acid Cys may be in the oxidized state forming

S-S-bridges, in particular a light chain variable domain comprising a polypeptide of the amino acid sequence 136 to 240 of SEQ ID NO:4, wherein the amino acid Cys may be in the oxidized state forming S-S-bridges.

For example, amino acids within the framework regions may be replaced by other amino acids or deleted as detailed above for the heavy chain.

Especially preferred is a chimeric protein comprising a single-chain recombinant antibody wherein the heavy chain variable domain and the light chain variable domain are linked by way of a spacer group consisting of 10 to 30, e.g. about 15, amino acids, in particular a single-chain recombinant antibody comprising a polypeptide of the formula

$$FR_1\text{-}CDR_{1H}\text{-}FR_2\text{-}CDR_{2H}\text{-}FR_3\text{-}CDR_{3H}\text{-}FR_4\text{-}Sp\text{-}FR_6\text{-}CDR_{1L}\text{-}FR_7\text{-}CDR_{2L}\text{-}FR_8\text{-}CDR_{3L}\text{-}FR_9 \quad \text{(III)},$$

wherein the polypeptide chain is described as starting at the N-terminal extremity and ending at the C-terminal extremity and FR_1, CDR_{1H}, FR_2, CDR_{2H}, FR_3, CDR_{3H}, FR_4, FR_6, CDR_{1L}, FR_7, CDR_{2L}, FR_8, CDR_{3L} and FR_9 have the meanings as mentioned before and Sp is a peptide spacer as disclosed above.

The antigen binding domain may be tested for its specificity to a predefined tumor cell antigen by methods known in the art, for example by immunofluorescent staining of cells expressing high levels of the antigen, by immunoblotting either directly or by way of immunoprecipitation and protein blotting of the immunocomplexes, or by another immunoassay such as binding, crossinhibition or competition radio- or enzyme immunoassay. The binding affinity of the antigen binding domain may be determined using a suitable quantitative assay which can easily be established by a person with ordinary skill in the art based on known techniques and principles. If desired, the affinity of the antigen binding domain may be compared to the affinity of a suitable reference antibody, e.g. the "parental" monoclonal mouse antibody it is derivable from.

Additionally to the antigen binding domain the chimeric protein of the invention comprises a hinge region which is inserted as a short, flexible tether between the antigen binding domain and the ζ domain. The hinge region is a peptide comprising from about 40 to about 200 naturally occurring amino acids, preferably from about 60 to about 190 amino acids. Preferably, the hinge region in the chimeric protein according to the

invention is an immunoglobulin-like hinge region, e.g. a hinge region derivable from the CD4 molecule, such as the D3D4 immunoglobulin domains (P.J. Maddon et al., Proc. Natl. Acad. Sci. USA. 84, 9155-9159 (1987)) or a hinge region derivable from the CD8α molecule, e.g. Lyt-2 (R. Zomoyska et al., Cell 43, 153-163 (1985); B.J. Classon et al., Int. Immunol. 4, 2, 215-225 (1992)). In the amino acid sequence set forth in SEQ ID No. 7 the hinge region (Lyt-2) extends from the amino acid at position 245 to the amino acid at position 304.

Additionally to the antigen binding domain and the hinge region the chimeric protein of the invention comprises a functional ζ domain contributing the transmembrane and the signalling domain of the chimeric protein. A functional ζ domain essentially comprises the transmembrane and the cytoplasmic domain of the ζ chain. The ζ domain mediated activation of the TCR by interaction of the antigen binding domain of the chimeric protein of the invention with a specific antigen triggers several signalling pathways, e.g. the ones mentioned above. According to the invention the ζ chain is of mammalian, particularly murine or human origin. Within the TCR ζ exists as a ζζ disulphide homodimer. A functional ζ domain is a protein which upon expression in T cell hybridomas deficient in endogenous ζ expression is capable of restoring in said hybridomas a functionally active TCR, e.g. in such a way that antigen-induced interleukin-2 secretion and growth stimulation are regained (S. Frank et al., Science 249, 174-177 (1990)). Examples of a functional ζ domain include molecules comprising amino acids 28 to 164 of the murine (A.M. Weissman, Science 239, 1018-1021 (1988)) and amino acids 28 to 163 of the human ζ chain (numbering according to A.M. Weissmann et al., Proc. Natl. Acad. Sci. USA 85, 9709-9713 (1988), Fig. 2, which is incorporated herein by reference). It is envisaged that a ζ protein as used for the purpose of the present invention is intended to include variants with the provision that these variants are functional. Preferred are variants of mammalian, particularly murine and human origin.

For example, a variant is a naturally occurring variant of the ζ molecule as found within a particular species. Such a variant may be encoded by a related gene of the same gene family or an allelic variant of a particular gene. The term "variant" also embraces a modified ζ molecule producible from a DNA which has been subjected to in vitro mutagenesis, with the provision that the protein encoded by the DNA has the functional activity of the authentic ζ molecule. Such modifications may consist in an addition, exchange and/or deletion of one or more amino acids, the latter resulting in shortened variants.

A preferred chimeric protein of the invention comprises a protein having the amino acid sequence depicted in SEQ ID No. 7.

Moreover, the invention relates to a polyclonal and monoclonal antibody specifically binding to a protein of the invention. Such an antibody is prepared according to conventional methods well known in the art.

The chimeric protein of the invention may be prepared by a process that is known per se, characterized in that suitable host cells as defined further below producing a protein of the invention, are multiplied in vitro or in vivo, and, if desired, the protein is isolated. Preferably, a protein of the invention is produced by a process comprising culturing suitable transduced CTL under conditions which allow the expression of the DNA construct encoding the protein and, optionally, performing an assay detecting the functionality of the protein. The invention further concerns a method for the manufacture of a chimeric protein of the invention comprising culturing a suitable host cell, particularly a CTL, which has been transduced with a vector comprising an expression cassette comprising a promoter and a DNA coding for said protein which DNA is controlled by said promoter under conditions which allow the expression of said DNA. A preferred chimeric protein of the invention is constructed to include a scFv, a hinge region and a functional ζ molecule. The process for producing the chimeric protein of the invention should yield the protein in an amount sufficient to enable the transduced host cell to lyse a target cell.

Suitable host cells include e.g. primary cytotoxic T lymphocytes (CD 8^+), CD 4^+ T helper cells and natural killer cells (NK). Preferred are mammalian cells, especially CTL of mammalian , particularly human origin.

As used hereinbefore or hereinafter, in vitro means ex vivo, thus including cell culture conditions.

For example, multiplication of mammalian cells in vitro is carried out in suitable culture media, which are customary standard culture media, such as Dulbecco's Modified Eagle Medium (DMEM) or RPMI 1640 medium, optionally replenished by a mammalian serum, e.g. fetal calf serum, or trace elements and growth sustaining supplements, e.g. feeder cells.

The invention also concerns a recombinant DNA or DNA construct suitable for manipulating the recognition specificity of T-lymphocytes. More specifically, the present invention provides a DNA construct capable of directing the synthesis of a chimeric protein comprising a recognition function, a hinge region and the ζ-chain as a signalling component of the TCR. In particular, the invention provides a DNA construct encoding a chimeric protein comprising an antigen binding domain, a hinge region and a ζ domain, particularly a DNA construct comprising at least one polynucleotide coding for a protein part designated as preferred hereinbefore or hereinbelow. In a preferred arrangement the antigen binding domain is conceived as the first part, the hinge region as the second part and the ζ chain as the third part.

By definition the DNAs of the invention include coding single stranded DNAs, double stranded DNAs consisting of said coding DNAs and DNA complementary thereto, or these complementary (single stranded) DNAs themselves.

Advantageously, the DNA construct of the invention comprises a fourth part which is located upstream of the first part (the antigen binding domain) and which encodes a leader peptide. Preferably, the fourth part of the DNA construct of the invention encodes a leader peptide of an immunoglobulin (Ig) gene, e.g. an Ig heavy chain leader peptide. The Ig heavy chain leader peptide promotes targeting of nascent polypeptides to the lumen of the endoplasmic reticulum; it is subsequently cleaved off and the protein is sorted through the Golgi and the membrane to its transmembrane location. Particularly preferred is a leader peptide having the sequence: Met-Ala-Trp-Val-Trp-Thr-Leu-Leu-Phe-Leu-Met-Ala-Ala-Ala-Lys-Val-Pro-Lys.

Preferred is a DNA comprising a DNA encoding the protein with the amino acid sequence depicted in SEQ ID No.7, e.g. a DNA having the nucleotide sequence depicted in SEQ ID No. 5. The DNA sequence set forth in SEQ ID No. 7 has the following features:
description of the sequence: 5'-EcoRI-IgH chain leader D6/12-scFv(FRP5):Lyt-2 hinge:-CD3 zeta(transmembrane (TM) and cytoplasmic (Cyt))-EcoRI-3'

5'EcoRI site:	position 1
3'RcoRI site:	position 1474
ATG initiation	position 40
TAA stop	position 1423
IGH chain leader	position 40-93

scFv(FRP5)	position 94-819
lyt-2 hinge insert	XbaI (position 819)- XbaI (position 1005)
zeta insert	XbaI (position 1005)- EcoRI (position 1474)

The present state of the art is such that a person with ordinary skill in the art will be able to synthesize a DNA molecule of the invention given the written information provided herein. A suitable method for obtaining a DNA construct of the invention involves methods well-known in the art comprising e.g. synthesis of a number of oligonucleotides, amplification of specific gene sequences, e.g. using PCR (polymerase chain reaction) technology, their splicing to give the desired DNA sequence and/or use of DNA restriction enzymes and ligases. A DNA of the invention may be synthesized by combining chemical with recombinant methods.

The invention further concerns a vector, such as a retroviral vector, comprising a DNA construct of the invention.

Additionally, the present invention provides a genetically engineered transduced CTL which is capable of destroying a targeted tumor cell in an MHC-independent and MHC-unrestricted manner. According to the present invention, the CTL produces the above-identified chimeric protein of the invention. The CTL is transduced with a DNA of the invention and thus is capable of expressing said DNA and of producing the protein encoded by said DNA. Destruction of the targeted tumor cell requires that the protein thus produced is functional, i.e. the antigen binding domain of said protein must be capable of recognizing and binding to the targeted tumor cell and the ζ domain must be capable of triggering the desired signal within the CTL. The CTL of the invention is cultured under conditions enabling (favoring) the expression of the introduced DNA and, if desired, assayed for the production thereof. Prolonged and elevated expression of said DNA is preferred.

Furthermore, the present invention provides a process for endowing a CTL with a defined, MHC-independent and MHC-unrestricted tumor cell specificity by introducing into said T-lymphocyte a DNA construct comprising a recognition function, a spacer domain and the ζ-chain as a signalling component of the TCR. The DNA construct may be introduced into the CTL by DNA-transfer methods apparent to those skilled in the art, e.g. by means

of a vector system, such as a viral or non-viral vector system. Suitable viral vectors include retroviral, adenoviral and adeno-associated viral vectors. The process is applicable to both in vivo and in vitro situations. In vitro application is preferred.

The T-lymphocyte is cultured under conventional conditions allowing the expression of said DNA construct and assayed for the production thereof. Prolonged and elevated expression of said DNA is preferred. Advantageously, CTL are cultured in the presence of IL-2. Transduced CTL of the invention may be selected for a suitable marker. For example, the transduced CTL may be selected for the cotransduced neo resistance marker if the DNA construct of the invention is transferred via a retroviral vector.

Moreover, the invention relates to a composition of matter comprising the transduced CTL of the invention. Such a composition comprises e.g. transduced CTL producing a protein of the invention together or in admixture with an acceptable, e.g. a pharmaceutically acceptable, carrier. Such a carrier may be a solid or liquid carrier. The composition may be used ex vivo, e.g. in order to kill preselected target cells in a composition (for example body liquid or tissue) removed from a patient's body. After the target cells have been killed (which should be checked) the composition is re-introduced into the patient's body. Thus the composition of the invention may be used for the treatment or adjuvant treatment of tumors.

Additionally, the present invention provides a process for lysing selected tumor cells comprising contacting said tumor cells to CTL producing the chimeric protein of the invention. In the process which is applicable to both in vitro and in vivo situations the tumor cell is targeted by the antigen binding domain which is part of the chimeric protein of the invention.

It is preferred to use the host's own CTL, particularly if the exposure and interaction is to occur in vivo, but, if appropriate, the CTL may also be derived from other sources. Other sources are e.g. tissue culture or another mammal of the same or different species.

CTL are found throughout the body of the mammal: in tissues, the lymphatic system and in the blood. Suitable CTL are selected and removed from the mammal. For example, CTL are selected as $CD8^+$ peripheral lymphocytes cultured in vitro in the presence of IL-2. Alternatively, unselected peripheral lymphocytes are used for gene transduction. If desired, the host may be treated such as to increase the number of stimulated CTL.

The invention further concerns a method of treating cancer comprising the use of the genetically engineered CTL of the invention. The method comprises exposing selected tumor cells to CTL producing the chimeric protein of the invention. An in vitro (meaning ex vivo) application of this method for promotion of CTL-mediated lysis may be in the selective treatment of tumor cells removed from a mammal, particularly a human, in the need of cancer treatment. An example would be to use the CTL of the invention to eliminate tumor cells from bone marrow removed from a patient, e.g. a patient undergoing radiation treatment prior, to re-introducing the bone marrow. As a consequence of the interaction of the tumor cells and the CTL of the invention the tumor cells are lysed. If the method of treating cancer is performed in vivo it may further comprise re-introducing the transduced CTL of the invention into the body of the mammal, particularly the human, to be treated. It is also envisaged that CTL expressing a DNA of the invention are produced by in vivo transduction of the DNA, e.g. in a mammal in need of cancer treatment.

The invention further concerns the CTL of the invention or a composition comprising said CTL for use in a method of treating cancer.

The invention particularly concerns the specific embodiments (e.g. protein, DNA, CTL and methods for the preparation thereof) described in the Examples. The following examples illustrate the invention but do not limit it to any extent.

Abbreviations: FCS: fetal calf serum; LDH: lactate dehydrogenase; mAb: monoclonal antibody; MoMLV: Moloney murine leukemia virus; MoMLV-LTR: Moloney murine leukemia virus-long terminal repeat, scFv: single chain antibody; SDS-PAGE: sodium dodecylsulfate polyacrylamide gel electrophoresis.

Materials and Methods

Cell Lines and Culture Conditions

Clone 96 (Cl96) is a H-2K^d-restricted cytotoxic T cell line derived from C57BL/6 mice (K. Eichmann et al., J. Immunol. 147, 2075-2081 (1991)). Cl96 and infectants are maintained in Dulbecco's modified Eagle's medium (DMEM, Gibco) supplemented with 10% FCS (Boehringer), 5 x 10^{-5} M 2-mercaptoethanol, 10 mM HEPES, 2 mM L-glutamine and 3% conditioned supernatant obtained from X63Ag8-653 plastocytoma cells transfected with the murine Il-2 cDNA (H. Karasuyama and F. Melchers, Eur. J. Immunol. 18, 97-104 (1988)). The human leukemic T cell line Jurkat, the retroviral

packaging cell lines ΩE (J.P. Morgenstern and H. Land, Nuc. Acids Res. 18, 3587-3596 (1990)) and P317 (A.D. Miller and G.J. Rosman, Biotechniques 7, 980-990 (1989)) and infectants and the murine fibroblast cell line transfected with the activated human erbB-2 receptor, NIH3T3#3.7 are cultured in DMEM supplemented with 10% FCS. HC11R1#11 is a mouse mammary epithelial cell line transfected with the human erbB-2 proto-oncogene (N.E. Hynes et al., Mol. Cell. Biol. 10, 4027-4034 (1990)) which is grown in RPMI 1640 (Gibco) supplemented with 10% FCS, 10 ng/ml epidermal growth factor and 5 μg/ml insulin.

<u>Example 1: Construction of the scFv(FRP5):hinge:zeta(ζ) cDNA</u>

A DNA consisting of a recognition function, a spacer domain and the ζ-chain as a signalling component of the TCR/CD3 receptor complex is constructed. The recognition function is contributed by a scFv domain. This domain is derived from the monoclonal antibody FRP5 (European patent application EP-A-502 812). FRP5 is specific for the extracellular domain of the erbB-2 receptor. The scFv (FRP5) comprises the variable domains of the heavy and light chains (V_H and V_L) of the monoclonal antibody (mAb) joined by a 15 amino acid linker sequence (SEQ ID NO:2). This scFv domain is able to recognize the extracellular domain of the erbB-2 receptor (W. Wels et al., Biotechnology 10, 1128-1132 (1992); W. Wels et al., Cancer Res. 15, 6310-6317 (1992)). A leader sequence from an immunoglobulin heavy chain is added to the N-terminus of the scFv domain. The scFv(FRP5) cDNA is ligated to a short linker sequence encoding 59 amino acids from the immunoglobulin-like hinge region of the CD8α gene (R. Zomoyska et al., Cell 43, 153-163 (1985)). The transmembrane and signalling domain are contributed by the ζ-chain of the TCR. This chain is responsible for the signal transduction following TCR activation.

The cDNA encoding the single chain antibody FRP5 specific for the extracellular domain of the erbB-2 molecule (SEQ ID NO:1) is subcloned into a plasmid containing an immunoglobulin heavy chain leader (L_{IgH}). Both, the ζ cDNA and the CD8α hinge cDNA are derived from total RNA of the cytotoxic T cell line C196 using a combination of reverse transcription and the polymerase chain reaction (RT-PCR). MoMLV reverse transcriptase is used for first strand cDNA synthesis. The reactions are primed with the 3' ζ-specific oligonucleotide 5813 (SEQ ID NO:6) or the 3' CD8α-specific oligonucleotide 8764 (SEQ ID NO:7), respectively. These cDNAs are used as PCR templates with the ζ primer pair 5812/5813 (SEQ ID NOs. 8 and 6) introducing a 5' XbaI site and a 3' HindIII/BglII site and the CD8α hinge primer pair 8763/8764 (SEQ ID NOs. 10 and 8)

introducing a XbaI site at both ends. The L_{IgH}-scFv(FRP5) DNA is ligated to the ζ cDNA starting from amino acid residue 28 (numbering according to A.M. Weissman et al., Science 239, 1018-1021 (1988)) using the XbaI site for the fusion. The CD8α hinge cDNA encoding amino acid residues 105 to 164 (numbering according to R. Zomoyska et al., Cell 43, 153-163 (1985)) is subsequently inserted into the XbaI site and checked for right orientation. The resulting scFv:hinge:ζ cDNA construct (SEQ ID No. 7) is confirmed by complete DNA sequencing and eventually subcloned into the unique EcoRI site of the pLXSN retroviral vector (A.D. Miller and G.J. Rosman, supra) resulting in the pL(scFv(FRP5):hinge:ζ)SN construct. The expression of the DNA is controlled by the 5' MoMLV-LTR. The plasmid also bears a selectable marker for neomycin resistance driven by the SV40 early promoter (SN).

Cloning of pL(scFv:D3/D4:ζ)SN

While the first molecular design includes the relatively short and flexible immunoglobulin hinge-like region of the murine Lyt-2 or CD8α molecule as tether, the second design encompasses the two membrane-proximal immunoglobulin-like domains designated as D3 and D4 of the murine L3T4 or CD4 molecule (S.J. Clark et al., Proc. Natl. Acad. Sci. USA 84, 1649-1653 (1987)) as a longer and more rigid spacer. D3/D4 encoding cDNA is obtained by PCR using pcd-L3T4 4.25 plasmid DNA (D.R. Littman and S.N. Gettner, Nature 325, 453-455 (1987)). The specific primer pair #8761/#8762 amplifies the coding sequences for amino acid residues 184-370 of the CD4 molecule (P.J. Maddon et al., Proc. Natl. Acad. Sci. USA 84, 9155-9159 (1987)) introducing XBaI restriction sites at both ends of the cDNA. The product is subcloned into the XbaI site of the pL(FZ)SN vector. After checking for the correct orientation of the insert, sequence identity of the resulting construct is confirmed by DNA sequencing. The structure of the pL(F4Z)SN is shown in Figure 1.

Primers for the amplification of the L3T4/CD4D3/D4 cDNA:
'Upstream' -5' Lyt-2/CD8-specific oligonucleotide #8761[1)]:
#8761: 5'-AGCTTCTAGAGTTTCAGAGCACAGCTCTCACGGCC-3'

'Downstream'-3'Lyt-2/CD8-specific oligonucleotide #8762[1)]:
#8762: 5'-TCGATCTAGAGTCTGGTTCACCCCTCTGG-3'

1) XbaI restriction sites are underlined.

Example 2: Expression of the scFv(FRP5):hinge:ζ DNA after retroviral gene transfer

The pLXSN vector system is capable of directing the efficient synthesis of the scFv(FRP5):hinge:ζ DNA after transduction into cytotoxic T cells and allows for G418 selection of infected cells. An established murine CTL line, C196, is infected with the pL(scFv(FRP5):hinge:ζ)SN construct of Example 1.

The ecotropic packaging cell line ΩE is transfected by calcium-phosphate precipitation with pL(scFv(FRP5):hinge:ζ)SN plasmid DNA. Transfected cells are stably selected in the presence of the neomycin analogue G418 (Geniticin, 1 mg/ml, Gibco). Viral supernatants are harvested after 48 hours from pools of G418 resistant helper cells and used to infect the amphotropic packaging cell line PA317 in the presence of 8 mg/ml polybrene. Clonal, high titer producer lines are derived by selection in 1.0 mg/ml G418 containing medium. Supernatants of these producer lines are used to infect C196 cells. Clones of infected cells selected for high expression of the scFv(FRP5):hinge:ζ DNA are derived and assayed for the production of chimeric cell surface proteins (Example 3). Clone CFYZ.1 is derived by growth in 1.0 mg/ml G418. Jurkat cells are infected using the same procedure, the clone JFYZ.4 is derived by growth in 2.0 mg/ml G418.

Example 3: Biochemical characterization of cell surface proteins

a) SDS-PAGE analysis of the chimeric scF(FRP5):hinge:ζ proteins produced by transduced CTL

Selected clones of Example 2 are cell surface biotinylated, lysed and immunoprecipitated with an anti-ζ mAb. For surface biotinylation, 3 x 10^7 viable cells are washed three times in biwa buffer (PBS, 1 mM $MgCl_2$, 0.1 mM $CaCl_2$) and resuspended in 1.5 ml Sulfo-NHS Biotin in biwa buffer (Pierce, 0.5 mg/ml). After incubating 15 min at 4°C, the reaction is quenched by addition of 25 mM L-lysine in biwa buffer. The cells are washed three times in quenching buffer (25 mM L-lysine in biwa buffer) and lysed in 1% NP- 40, 150 mM NaCl, 50 mM Tris/HCL pH 8.0, 5 mM EDTA, 1 mM PMSF containing buffer supplemented with a protease inhibitor cocktail. Postnuclear lysates are precleared overnight with Protein A Sepharose (Pharmacia). Immunoprecipitation is performed by addition of 3 mg of the ζ-specific mAb H146-968 which recognizes human and mouse COOH terminus of the ζ chain, incubated for 3 hours followed by 1 hour incubation with Protein A Sepharose. The preciptitate is washed four times in NET-TON (650 mM NaCl, 5 mM EDTA, 50 mM Tris/HCl, 0.5% Triton X-100, 1 mg/ml ovalbumin). For deglycosylation, precipitates are denatured in 5% SDS with or without 10%

2-mercaptoethanol at 100°C and incubated with 2.000 U PNGase F (Biolabs) for 1 hour at 37°C. Samples are boiled in either non-reducing or reducing Laemmli-sample buffer and electrophoresed through 5-20% SDS-PAGE gradient gels. The proteins are transferred to a PVDF membrane (Millipore) and blocked in PBS-T (PBS, 0.4% Tween-20) containing 5% skim milk powder (Fluka). The membrane is incubated for one hour with PBS-T containing horseradish peroxidase-streptavidin (HRP-Strep, Southern Biotechnology, 1:5.000). After washing the membrane four times for 7 min in PBS-T, the blot is developed using the ECL-chemoluminescence reagent (Amersham). The SDS-PAGE analysis of the immunoprecipitates under reducing conditions reveals a series of bands with an apparent molecular weight of about 48-65 kDa from lysates of infected cells (clone CFYZ.1), but not in lysates of the parental cells (C196 cells). The 48 kDa band corresponds to the scFv(FRP5):hinge:ζ protein with a calculated molecular weight of 48.7 kDa. The amino acid sequence of said protein is depicted in SEQ ID NO:5. In said sequence listing the recognition part derived from mAb FRP5 extends from the amino acid at position 6 (Gln) to the amino acid at position 240 (Ile), the hinge region derived from CD8α extends from the amino acid at position 245 (Ile) to the amino acid at position 304 (Phe) and the ζ chain extends from the amino acid at position 307 (Asp) to the amino acid at position 443 (Arg). The higher molecular weight species arise as a consequence of complex glycosylation of the scFv and the hinge region. Deglycosylation with the endoglycosidase PNGase F results in a simplified protein pattern and the reduction of the apparent molecular weight to about 47 kDa. The endogenous ζ-chain is detected as a 16 kDa band (16.3 kDa predicted) in uninfected and infected cells. When the SDS-PAGE analysis is carried out under non-reducing conditions, both disulfide-linked scFv:hinge:ζ homodimers with an apparent molecular weight of about 96 kDa as well as heterodimers of scFv(FRP5):hinge:ζ molecules with the endogenous ζ with an apparent molecular weight of about 64 kDa are observed. PNGase F treatment slightly reduced the molecular weights of these two bands. The detected 32 kDa band corresponds to endogenous ζ-ζ homodimers of the CTL.

b) Flow cytometric analysis of scFv(FRP5):hinge:ζ protein producing T cells
Cell surface expression and erbB-2 receptor binding ability of the scFv(FRP5):hinge:ζ protein in transduced C196 CTL and in transduced Jurkat cells are confirmed by flow cytometry.
Single-cell suspensions of 5 x 10^5 viable cells (Jurkat cells, JFYZ.4 cells, C196 cells, CFYZ.1 cells) are stained with the purified extracellular domain of the erbB-2 protein (erbB-2^{ecd}, expressed in Sf9 insect cells using a baculovirus expression vector; Disis et

al., Cancer Res. 54, 16-20 (1994)) for 1 hour followed by the FITC-conjugated anti-erbB-2 monoclonal antibody FSP77 (European patent application EP-A-502 812) for 45 min at 4°C in 100 μl PBS containing 1% BSA and 0.1% sodium azide. FSP77 also is specific for the extracellular domain of the erbB-2 receptor, but recognizes a different epitope from mAb FRP5 (I.M. Harwerth et al., J. Biol. Chem. 21, 15160-15167 (1992)). Ten thousand forward scatter/side scatter gated viable cells are acquired and analysed with a flow cytometer revealing binding of the purified, soluble extracellular domain of the erbB-2 receptor to the transduced T cells JFYZ.4 and CFYZ.1 but not to non-infected Jurkat or Cl96 cells.

The hinge region provides flexibility and accessibility to the scFv moiety and is a necessary prerequisite for the binding of the extracellular domain of the erbB-2 receptor to the scFv domain. Insertion of the CD4 D3D4 also allows binding. A construct in which a direct fusion, without a hinge region or spacer, of the scFv domain to the ζ-chain is tested, results in a surface receptor which cannot bind to the erbB-2 protein.

Example 4: Signal transduction of the scFv(FRP5):hinge:ζ fusion protein

The intracellular calcium (Ca^{2+}) concentration of T cells loaded with a suitable calcium-chelating fluorescent dye is measured after incubation with the soluble erbB-2 receptor. For this purpose cultured JFYZ.4 infectants and Jurkat cells are suspended at 1 x 10^7/ml in RPMI 1640 supplemented with 2% FCS and 5 mM Indo-1/AM (Calbiochem) (M. Lopez et al., Cytometry 10, 165-173 (1989)) and rotated for 45 min at 37°C. After washing twice, 3 x 10^5 cells are incubated on ice with 2 mg purified erbB-2^{ecd}. Triggering is performed at 37°C by simultaneous administration of 5 mg anti-erbB-2 mAb FSP77 followed by crosslinking with a goat anti-mouse Ig antiserum (GαM Ig, Southern Biotechnology). As a control, cells are triggered by addition of anti-human CD3ε mAb (Serva) and GαM Ig. Calcium flux is monitored for 15 min on a flow cytometer by measuring emission at 405 and 525 nm.

Crosslinking results in a rapid increase of intracellular calcium in JFCZ.4 cells but not in parental Jurkat cells comparable to that obtained by crosslinking the CD3 complex with an anti-CD3ε mAb in non-infected cells. This indicates that intracellular signalling is triggerred upon crosslinking of the scFv(FRP5):hinge:ζ protein via an extracellular ligand domain and that the scFv(FRP5):hinge:ζ protein is functionally active.

Example 5: In vitro cytotoxicity assay

The cytolytic activity of infected Cl96 (CFYZ.1) cells is determined in vitro.

Oncogenically transformed mouse NIH/3T3 fibroblasts and HC11 epithelial cells expressing the human erbB-2 receptor (N.E. Hynes et al., supra)) are employed as target cells. The release of LDH from these cells is used as a measure of cell lysis (T. Decker and M.L. Lohmann-Matthes, J. Immunol. Methods 115, 61-69 (1988)).
The cytotoxicity assay is performed in phenol red free medium supplied with 4% conditioned supernatant containing recombinant murine Il-2 (rmIl-2, see above). A constant number of target cells (7.500/well) is added to a serial 2-fold dilution of effectors (CFYZ.1 cells) followed by an eight hour incubation at 37°C and 5% CO_2. All dilutions are performed in triplicates. The LDH content of a 50 µl aliqout of the supernatant is assayed using the CytoTox 96 assay (Promega) (T. Decker and M.L. Lohmann-Matthes, supra). The LDH activity measured after lysis of target cells with 0.4% Triton X-100 is considered as 100%. The measured experimental values are corrected for the spontaneous release of LDH from effector and target cells. Infected Cl96 cells expressing the scFv(FRP5):hinge:ζ construct efficiently lyse erbB-2 expressing NIH/3T3 cells or HC11 cells at effector to target ratios between 1 and 10. Lysis of the epithelial and fibroblast target cells ttransfected with the human erbB-2 receptor occurs in a non MHC-restricted manner indistinguishable from normal antigen-specific cellular cytotoxicity. In contrast, no cell lysis is observed when the parental Cl96 cells are used as effectors. The mAb FRP5 and the derived scFv domain are specific for the human erbB-2 molecule and do not recognize the mouse homologue which is expressed at low levels on both cell lines. For this reason, no cell lysis is observed when untransfected NIH/3T3 cells or HC11 cells are incubated with the scFv(FRP5):hinge:ζ construct expressing T cells.

Example 6: In vivo anti-tumor activity

Two experimental schedules are used to assess the anti-tumor activity of the transduced CTL (infected Cl96 cells) in vivo. In the first schedule, 5 x 10^5 NIH3T3#3.7 tumor cells are mixed with 5 x 10^6 CFYZ.1 cells or parental Cl96 cells (effector to target ratio of 1:10) in 0.1 ml culture medium and immediately injected subcutaneously (s.c.) into the right flank of Balb/c nude mice (H.J. Winn, J. Immunol. 86, 228-234 (1961)). The growth of the tumors is followed by caliper measurements. NIH3T3#3.7 tumor cells alone are injected as a control. Each group consists of five animals. In the second schedule, Balb/c nude mice are inoculated s.c. into the right flank with 4 x 10^5 NIH3T3#3.7 tumor cells. On day 4 and 5, when tumors are palpable, parental Cl96 cells and CFYZ.1 cells are injected intravenously into the tail vein (1 x 10^7 cells in 0.2 ml culture medium). 500 U of rhIl-2 (Hoffmann-La Roche) in 0.2 ml PBS are administered intraperitoneally on days 4, 5 and 6. The growth of the tumors is followed by caliper measurements. NIH3T3#3.7 cells

without Il-2 and with Il-2 are injected as controls. Each group consists of five animals. NIH/3T3 cells transformed with the human erbB-2 oncogene lead to the rapid formation of tumors after subcutaneous injection into athymic Balb/c nude mice. The simultanous administration of CFYZ.1 infectants and tumor cells completely suppresses tumor formation for up to 7 days. Administration of the uninfected parental Cl96 cells, however has no effect on tumor cell growth. A similar result is obtained when nude mice are inoculated first with NIH/3T3-erbB-2 tumor cells and subsequently treated with CFYZ.1 cells in combination with exogenous Il- 2. The administration of the transduced CTL strongly retards the growth of the tumor cells over a course of seven days thus showing a systemic in vivo effect. The cells have the capability to home the tumor, to be activated and display their cytolytic activity when administered at a different site.

These results show that the specificity and thus the cytolytic effector machinery of the transduced CTL can be efficiently redirected towards a predefined surface antigen, the erbB-2 receptor, which plays an important role in the etiology of many human adenocarcinomas including breast, ovarian, gastric and colon cancer. Therefore the principle of targeted T cell action is conceived as a useful therapy approach and generally applicable for the elimination of tumor cells which express a surface antigen at higher levels than normal cells. The design permits the generation of CTL with many desired specificities by exchanging the scFv moiety and replacing it with any existing antigen recognition function derived from a specific monoclonal antibody. The use of efficient transfer systems, e.g. retroviral vectors, allows the transfer of scFv:hinge:ζ DNAs into cell types which are not easily transfectable.

<u>Deposition data:</u>

Hybridoma cell lines producing antibodies FRP5, FSP16, FSP77 and FWP51 have been deposited with the European Collection of Animal Cell Cultures (ECACC, PHLS Centre for Applied Microbiology & Research, Porton Down, Salisbury, UK) on November 21, 1990 under accession numbers 90112115, 90112116, 90112117 and 90112118, respectively.

<u>Brief Description of the Figure:</u>

Figure 1: Structure of the pL(F4Z)SN retroviral vector. A cDNA encoding amino acid residues number 184 - 370 of the CD 4 immunoglobulin like D3 and D4 domains is derived by PCR and subcloned inot the XbaI site of the PL(FX)SN vector. Amino acid sequences of the fusion boundaries are shown in the single letter code.